-continued

```
<211> LENGTH: 15
<212> TYPE: RNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic terminator sequence

<400> SEQUENCE: 17

cuuucugcgu uuaua                                                          15


<210> SEQ ID NO 18
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic terminator sequence flanked on the
      5' end by the XhoI restriction site and the tet repressor binding
      site and on the 3' end by the BamHI restriction site
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(12)
<223> OTHER INFORMATION: "nnn" is the sequence to which the tet
      repressor binds

<400> SEQUENCE: 18

agatctccan nnctttctgc gtttatagga tcc                                     33


<210> SEQ ID NO 19
<211> LENGTH: 90
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli
<220> FEATURE:
<223> OTHER INFORMATION: Dre Y324F knockout
<220> FEATURE:
<221> NAME/KEY: mutation
<222> LOCATION: (46)..(46)
<223> OTHER INFORMATION: Dre Y324F knockout

<400> SEQUENCE: 19

ttatgcaaga gggcacctgg aaaaaactga gaccctgatg cgctttctgc gtcgtggtgg        60

cgtaagcgtc ggcgctaata gccggctgat                                         90


<210> SEQ ID NO 20
<211> LENGTH: 90
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 20

ttatgcaaga gggcacctgg aaaaaactga gaccctgatg cgctatctgc gtcgtggtgg        60

cgtaagcgtc ggcgctaata gccggctgat                                         90
```

What is claimed is:

1. A recombinant nucleic acid comprising a nucleotide sequence comprising a plurality of constructs, wherein each construct independently comprises a nucleotide sequence of interest flanked by a pair of recombinase recognition sequences.

2. The recombinant nucleic acid of claim 1 wherein each construct independently further comprises one or more genes encoding a recombinase capable of recognizing the pair of recombinase recognition sequences of the construct.

3. A recombinant nucleic acid comprising a first construct and a second construct; wherein the first construct comprises a nucleotide sequence encoding a first recognition sequence of a first recombinase, a second recognition sequence of the first recombinase, and a first nucleotide sequence of interest located between the first and second recognition sequence of the first recombinase; wherein the second construct comprises a nucleotide sequence encoding a first recognition sequence of a second recombinase, a second recognition sequence of the second recombinase, and a second nucleotide sequence of interest located between the first and second recognition sequence of the second recombinase; wherein the second construct is located downstream of the first construct; wherein the first recombinase and the second recombinase do not cross react with the recognition sequence of the other.